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181 CTGAGCCCCCTTCACATGATCCTTGGAGGAATCATTGGGTGCTGCTGTTTACGGGGTTTGTGTGGGCAGCCACACATAAAGACATCCTC
   L S P F N M I L G G I I V V L V F T G F V W A A H N K D I L
271 CGCCGGATGAAGAAGCAGTACCCAACGGCCTTTGTCATGGTGGTCATGCTAGCCAGCTACTTCCCTCATATCCATGTTTGGGGGTGTCATG
   R R M K K Q Y P T A F V M V V M L A S Y P L I S M F G G V M
361 GTCTTTGTGTTTGGCATCACGTTTCCCTTATTGTTGATGTTTCATCCATGCATCCCTGAGACTTCGAAACCTCAGGAACAACTGGAAAT
   V F V F G I T F P L L L M F I H A S L R L R N L R N K L E N
451 AAATGGAGGGGANTAGGCTTGAAGAAAACGCCGATGGGCATCATCCTGGATGCCTTGGAAACAGCAGGAGACAGCATCAATAAATTGCT
   K M E G I G L K K T P M G I I L D A L E Q Q E D S I N K F A
541 GACTACATCAGCAAGCCAGGGAGTAA
   D Y I S K A R E *

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Supplement 1. Nucleotide and amino acid sequence of GTRAP3-18. Lines 1-4: putative transmembrane domains, double lines: potential protein kinase-dependent phosphorylation sites (S/T-X-K/R). GenBank accession number for GTRAP3-18 is AF240182.

Fig. 1

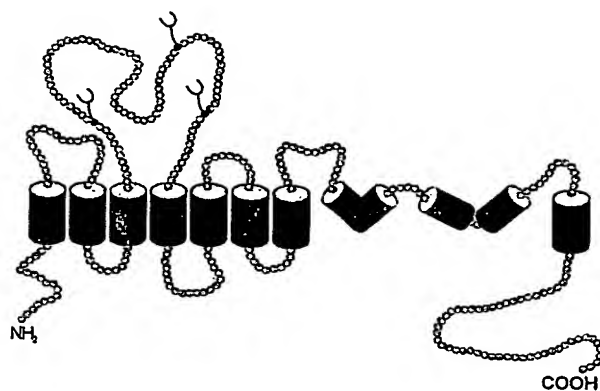


Fig. 2

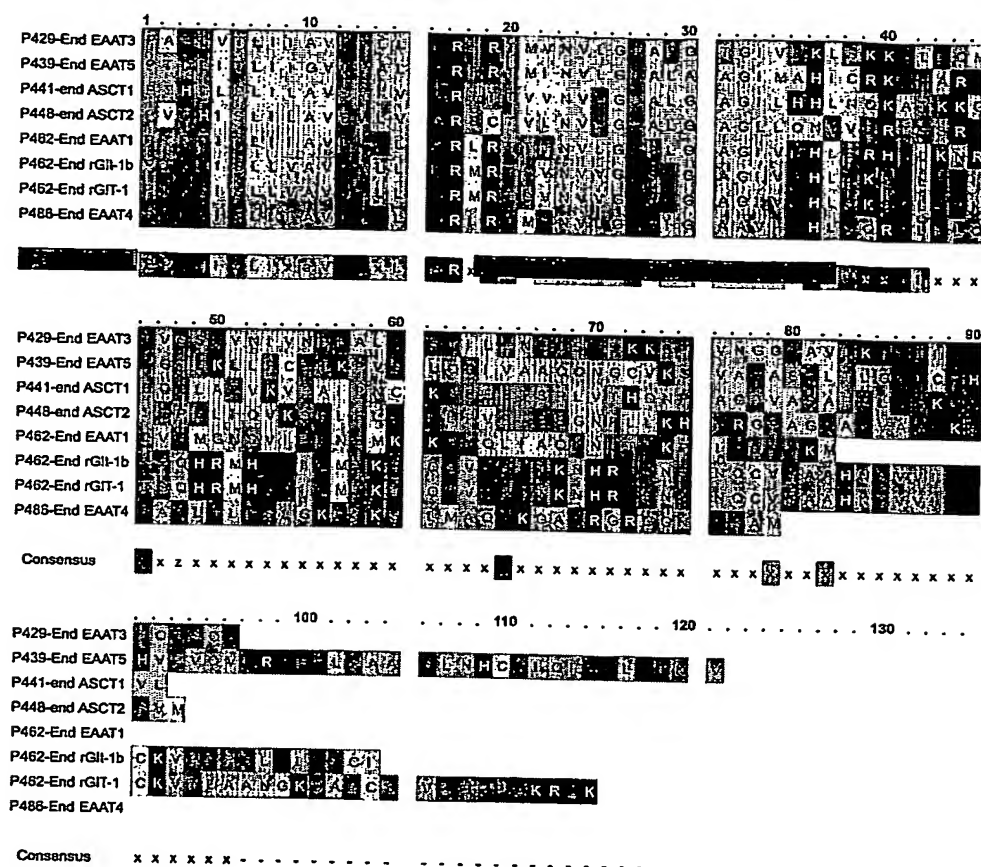
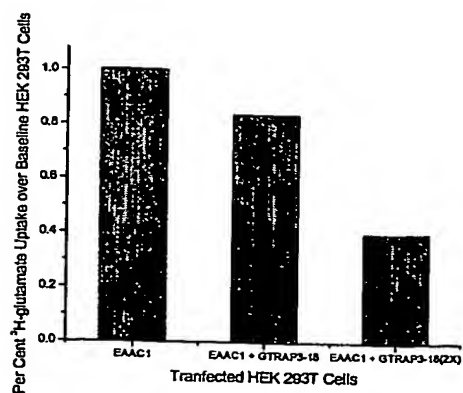
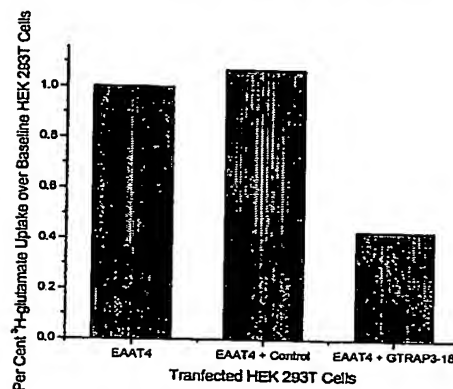
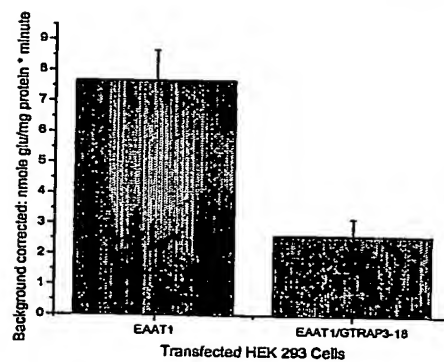
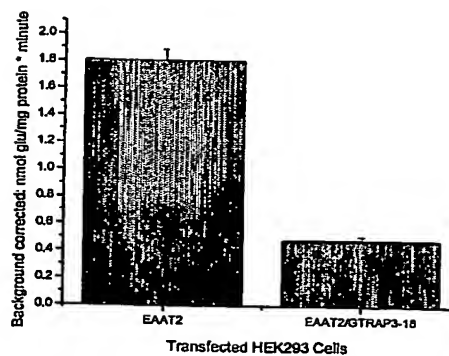
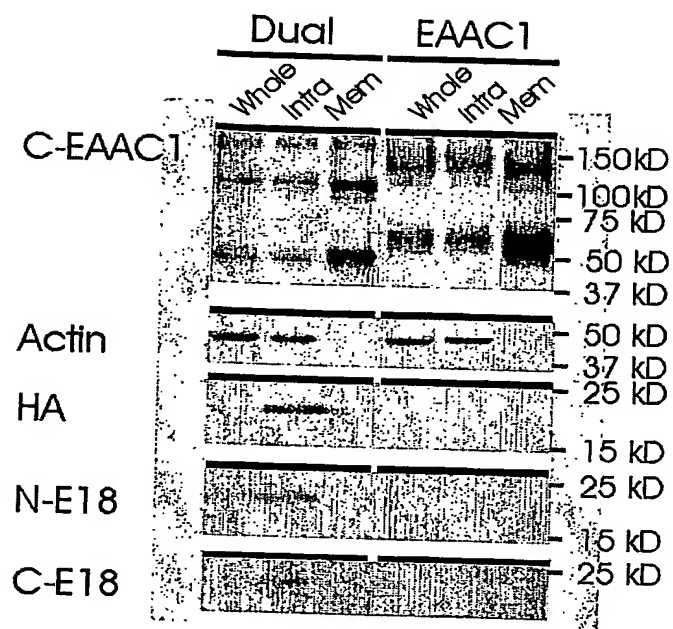


Fig. 3

Fig. 4A**Fig. 4B****Fig. 4C****Fig. 4D**

**Fig. 5**

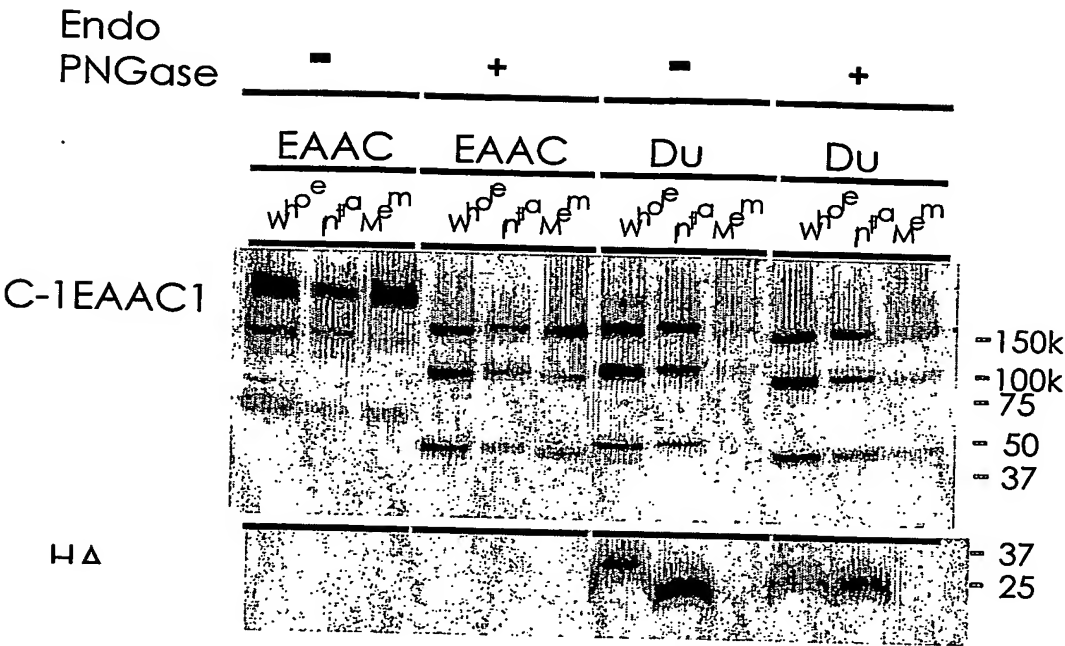


Fig. 6A

Fig. 6B



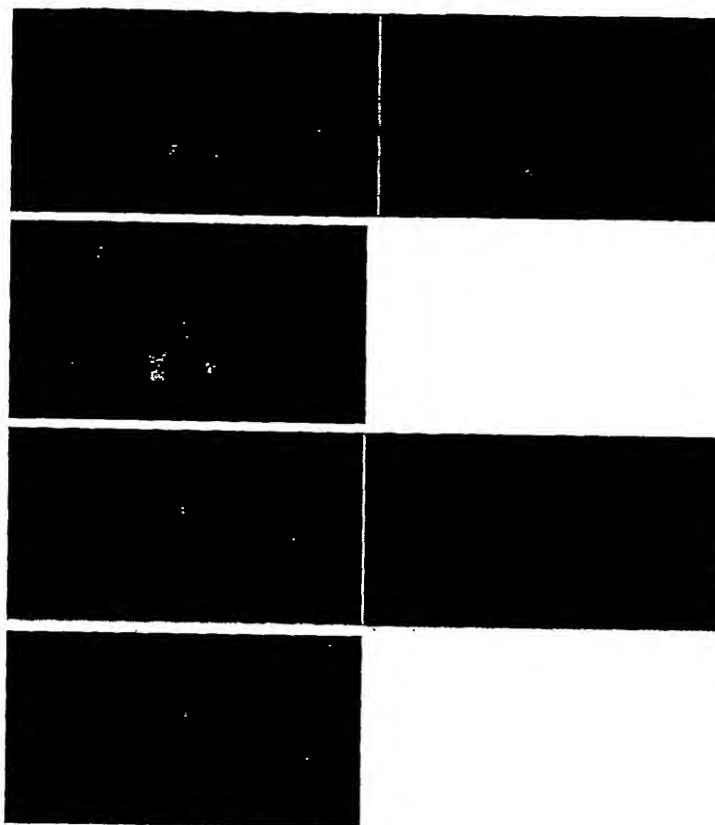


Fig. 7